

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 101738,404

Source: _____

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/738,404

DATE: 02/18/2005

TIME: 11:13:47

Input Set : N:\CrF3\RULE60\10738404.raw.txt
 Output Set: N:\CRF4\02182005\J738404.raw

1 <110> APPLICANT: Philip E. Thorpe
 2 Rolf A. Brekken
 3 <120> TITLE OF INVENTION: ANTIBODY CONJUGATE METHODS FOR SELECTIVELY INHIBITING VEGF
 4 <130> FILE REFERENCE: 4001.002585
 5 <140> CURRENT APPLICATION NUMBER: US/10/738,404
 6 <141> CURRENT FILING DATE: 2003-12-17
 7 <150> PRIOR APPLICATION NUMBER: US/09/561,005
 8 <151> PRIOR FILING DATE: 2000-04-28
 9 <150> PRIOR APPLICATION NUMBER: 60/131,432
 10 <151> PRIOR FILING DATE: 1999-04-28
 11 <160> NUMBER OF SEQ ID NOS: 44
 12 <170> SOFTWARE: PatentIn Ver. 2.0
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 2149
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Homo sapiens
 18 <400> SEQUENCE: 1
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 21 aaaattttaa aatttttagaa caaagctaac aaatggctag ttttctatga ttcttcttca 180
 22 aacgctttct ttgaggggga aagagtcaaa caaacaagca gtttacacgt aaataaagaa 240
 23 ctatgttttag aggtcagaag aaaggagcaa gtttgcgag aggcacggaa ggagtgtgct 300
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 25 ggggtcagca atcagcggccg aagtccagaa aacagtggga gaagatataaa ccggattcaa 420
 26 catggcaat gtgcctacac tttcattctt ccagaacacg atggcaactg tcgtgagagt 480
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 28 ttcttccc agaaacttca acatctggaa catgtgatgg aaaattatac tcagtgctg 600
 29 caaaaacttg agaattacat tggaaaac atgaagtccg agatggccca gatacagcag 660
 30 aatgcagttc agaaccacac ggctaccatg ctggagatag gaaccagcct cctcttcag 720
 31 actgcagagc agaccagaaa gctgacagat gttgagaccc agtactaaa tcaaacttct 780
 32 cgacttgaga tacagctgct ggagaattca ttatccacct acaagctaga gaagcaactt 840
 33 cttaacacaga caaatgaat cttaagatc catggaaaaa acagttttatt agaacataaa 900
 34 atcttagaaa tggaaaggaaa acacaaggaa gagttggaca ctttaaagga agagaaagag 960
 35 aaccttcaag gcttggttac tcgtcaaaca tatataatcc aggagctgga aaagcaatta 1020
 36 aacagagcta ccaccaacaa cagtgtcctt cagaagcgc aactggagct gatggacaca 1080
 37 gtccacaacc ttgtcaatct ttgcactaaa gaagggttt tactaaaggg agggaaaaaga 1140
 38 gaggaagaga aaccatttag agactgtgca gatgtatatc aagctggtt taataaaagt 1200
 39 ggaatctaca ctatttatata taataatatg ccagaaccca aaaagggttt ttgcaatatg 1260
 40 gatgtcaatg ggggagggtt gactgtataa caacatctgt aagatggaaag tctagatttc 1320
 41 caaagaggct ggaaggaata taaaatgggt tttggaaatc cttccgggtga atattggctg 1380
 42 gggaatgagt ttatgttgc cattaccagt cagaggcagt acatgctaag aattgagtt 1440
 43 atggactggg aaggaaaccg agcttattca cagtatgaca gattccacat aggaatgaa 1500
 44 aagcaaaact ataggttga tttaaaaggt cacactggga cagcaggaaa acagagcagc 1560

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46 aaatgtgccccc tcatgttaac aggaggatgg tgggttgatg ctgtggccc ctccaatcta 1680
47 aatgaatgt tctatactgc gggacaaaac catggaaaac tgaatggat aaagtggcac 1740
48 tactcaaag ggcggcaggta ctccttacgt tccacaacta tggatgattcg accttttagat 1800
49 ttttggaaagc gcaatgtcag aaggcattat gaaagcaaca aagaaatccg gagaagctgc 1860
50 caggtgagaa actgtttgaa aacttcagaa gcaaacaata ttgtctccct tccagcaata 1920
51 agtggtagtt atgtgaagtc accaagggttc ttgaccgtga atctggagcc gttttagttc 1980
52 acaagagtct ctacttgggg tgacagtgc cacgtggctc gactatagaa aactccactg 2040
53 actgtcgggc tttaaaaagg gaagaaaactg ctgagcttgc tggcttcaa actactactg 2100
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59 <213> ORGANISM: Homo sapiens
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64 20 25 30
65 Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
66 35 40 45
67 Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
68 50 55 60
69 Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
70 65 70 75 80
71 Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
72 85 90 95
73 Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
74 100 105 110
75 Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
76 115 120 125
77 Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
78 130 135 140
79 Leu Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu
80 145 150 155 160
81 Ile Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln
82 165 170 175
83 Leu Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser
84 180 185 190
85 Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
86 195 200 205
87 Leu Asp Thr Leu Lys Glu Glu Lys Glu Asn Leu Gln Gly Leu Val Thr
88 210 215 220
89 Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gln Leu Asn Arg Ala
90 225 230 235 240
91 Thr Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp
92 245 250 255
93 Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
94 260 265 270

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95 Lys Gly Gly Lys Arg Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp
 96 275 280 285
 97 Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile
 98 290 295 300
 99 Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn
 100 305 310 315 320
 101 Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp
 102 325 330 335
 103 Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser
 104 340 345 350
 105 Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln
 106 355 360 365
 107 Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg
 108 370 375 380
 109 Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
 110 385 390 395 400
 111 Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
 112 405 410 415
 113 Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
 114 420 425 430
 115 Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp
 116 435 440 445
 117 Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
 118 450 455 460
 119 Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys
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 132 agcaggactg ttcttccac tgcaatctga cagtttactg catgcctgga gagaacacag 180
 133 cagaaaaaac caggttgct actggaaaaa gaggaaagag aagacttca ttgacggacc 240
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 139 tgtcagagg gacgcgccgc tgcataacga tgactcggtc cagaggctgc aagtgctgga 600
 140 gaacatcatg gaaaacaaca ctcagtggtc aatgaagctt gagaattata tccaggacaa 660
 141 catgaagaaa gaaatgttag agatacagca gaatgcgtc cagaaccaga cggctgtat 720
 142 gatagaataa gggacaaacc tggtaacca aacagctgag caaacgcgga agttaactga 780
 143 tgtgaaagcc caagtattaa atcagaccac gagacttcaa cttcagctct tggacactc 840
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 147 ttccatcatt gaagaactag aaaaaaaaaat agtactgccc acggtaata attcagtct 1080
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 152 tattcagcga cgtgaggatg gcagcgttga tttcagagg acttggaaag aatataaaagt 1380
 153 gggatttggtaacccttcag gagaatattt gctggaaat gagttgtt cgcaactgac 1440
 154 taatcagcaa cgctatgtc taaaataca ccttaaagac tgggaaggga atgaggctta 1500
 155 ctcatgtat gaacatttct atctctcaag tgaagaactc aattataga ttcaccttaa 1560
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 157 cacaaggat ggagacaacg acaaatgtat ttgcaatgt tcacaaatgc taacaggagg 1680
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 165 gaatcagact gacagttac agacgctgct gtcacaacca agaatgttat gtgcaagttt 2160
 166 atcagtaaat aactggaaaa cagaacactt atgttataca atacagatca tcttggaaact 2220
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 171 <212> TYPE: PRT
 172 <213> ORGANISM: Homo sapiens
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 177 20 25 30
 178 Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
 179 35 40 45
 180 Glu Met Asp Asn Cys Arg Ser Ser Ser Ser Pro Tyr Val Ser Asn Ala
 181 50 55 60
 182 Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
 183 65 70 75 80
 184 Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys
 185 85 90 95
 186 Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile
 187 100 105 110
 188 Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly
 189 115 120 125
 190 Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp
 191 130 135 140
 192 Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu
 193 145 150 155 160
 194 Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp

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196	Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu		
197	180	185	190
198	Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser		
199	195	200	205
200	Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn		
201	210	215	220
202	Ser Ile Ile Glu Glu Leu Glu Lys Ile Val Thr Ala Thr Val Asn		
203	225	230	240
204	Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn		
205	245	250	255
206	Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ser Ala Lys Asp Pro Thr		
207	260	265	270
208	Val Ala Lys Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe		
209	275	280	285
210	Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Thr Phe Pro Asn		
211	290	295	300
212	Ser Thr Glu Glu Ile Lys Ala Tyr Cys Asp Met Glu Ala Gly Gly		
213	305	310	315
214	Gly Trp Thr Ile Ile Gln Arg Arg Glu Asp Gly Ser Val Asp Phe Gln		
215	325	330	335
216	Arg Thr Trp Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu		
217	340	345	350
218	Tyr Trp Leu Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg		
219	355	360	365
220	Tyr Val Leu Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr		
221	370	375	380
222	Ser Leu Tyr Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg		
223	385	390	395
224	Ile His Leu Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile		
225	405	410	415
226	Ser Gln Pro Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys		
227	420	425	430
228	Cys Ile Cys Lys Cys Ser Gln Met Leu Thr Gly Trp Trp Phe Asp		
229	435	440	445
230	Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln		
231	450	455	460
232	Asn Thr Asn Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser		
233	465	470	475
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/18/2005
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Input Set : N:\CrF3\RULE60\10738404.raw.txt
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3

VERIFICATION SUMMARY

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L:421 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12